

**Table S3.** PCR primer sequences used in this study.

Gene	Description	Primer		Product size (bp)	Reference
		Direction	Sequence		
<i>escN</i>	ATPase of T3SS	F	CGCCTTTACAAGATAGAAC	856	1
		R	CATCAAGAATAGAGCGGAC		
<i>espA</i>	Component of T3SS	F	ACTCGGTGTTTCAGGCTGC	445	2
		R	TGAAATAGTTCTATATTG		
<i>Ler</i>	LEE-encoded regulator	F	ATGCGGAGATTATTATTATG	393	3
		R	ATGTTAAATATTTTCAGCGG		
<i>lifA/efa1</i>	adhesin protein/lymphostatin	F	AGAATGGAAGATCACACCAG	310	4
		R	ATAATGCCTTCATCCACAC		

TTSS: Type 3 secretion system; LEE: Locus of Enterocyte Effacement

1. Kyaw CM, De Araujo CR, Lima MR, Gondim EG, Brigido MM, Giugliano LG. 2003. Evidence for the presence of a type III secretion system in diffusely adhering *Escherichia coli* (DAEC). *Infect Genet Evol*. 3:111-117.
2. Kobayashi H, Shimada J, Nakazawa M, Morozumi T, Pohjanvirta T, Pelkonen S, Yamamoto K. 2001. Prevalence and characteristics of shiga toxin-producing *Escherichia coli* from healthy cattle in Japan. *Appl Environ Microbiol* 67:484-489.
3. Sharma VK, Zuerner RL. 2004. Role of *hha* and *ler* in transcriptional regulation of the *esp* operon of enterohemorrhagic *Escherichia coli* O157:H7. *J Bacteriol* 186:7290-7301.
4. Narimatsu H, Ogata K, Makino Y, Ito K. 2010. Distribution of non-locus of enterocyte effacement pathogenic island-related genes in *Escherichia coli* carrying *eae* from patients with diarrhea and healthy individuals in Japan. *J Clin Microbiol* 48:4107-4114.